

Fig. 1

IDENTIFIED LAB mRNA SEQUENCES

CGGGAGCTTGAAGGACACAAGAATGGGAGGAAAGGCGGACTCTCAGGAAC (Ribosome Binding Site)
 TTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACAT (Start Codon)
 CTGTAGCTGTCGTTTGGTTGATCTTGTTGACTATGAGGAAGTTCTAGGA
 AAAC TAGGAATCTATGATGCTGATGGTGATGGAGATTTTGTGTGGATGA
 TGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAG
 TCCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCCGAGGAGCAGGTTCCCT
 GTGGAGGCAGAACCCAGAAATATCGAAGATGAAGCAAAAGAACAATTCA
 GTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACT
 TGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAG
 TTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGA
 AGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTT
 CACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAAT
 CCAGATTCCAGTGAACCACTAGTAGAAGATGAAAGATTGCACCATGATAC
 AGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTC
 TAGAAAATGAAGGGATAGAAAATCACAGAAGTAACTGCTCCCCCTGAGGAT
 AATCCTGTAGAAGATTACAGGTAATTGTAGAAGAAGTAAGCATTTTTTCC
 TGTGGAAGAACAGCAGGAAGTACCACCAGATACTTAAAGCTTCAAAAAGA (Stop Codon)
 CTGCCCCCTACCACCACAGGAGGACCAGCCTAACCATACGCTCCAAAAGAT
 GGCTGTGATAGATCTTGTGAAGCAATTACTGAGCAGATCAAGATCTTTGG
 GAAGGAACACTAAAGATGTTTTGAATGAATTATAGTCCACTGGCATTTTA
 GTGTATTTTTTTTTCTTTT TAGAAACACACATTTCTAAAAATGTCATGTT
 ACATTCTGCATGTCCCTTTTGATAGCATTAGTGGATCCATTGGATTTCT
 TTTTCTTTTTGTGAGACAGCTTTTAGTCTTACCTGAATTTATGTGTGTT (Instability Sequence)
 TTTCCGACAGTGGTTAATAATTATATTGGTGATGTAGCAGCAATTGTGTT
 GGCAGGTTTTTCATATATTATTAGTAATTAACACTAACTGTTGGACTGAC
 TTGTGTACACTGTGTTAAACATGATTTAAAGCTATTAAGAGTACTTTGT (Instability Sequence)
 GTTAGCACTCTTAAAAACGCTAACAGAGATCATCATTAGCTGTGAAGATT
 TGAGTTGTATATACCTGCACTGATATTCTTATCAAAAATTTCTACATTAG
 CTTTAAGTGTTTCAGATTAACACTTTTGAAACCTTTGTAGCTTTTAGCTGA
 TTAATTAGAAAAAATAATTTTCACTGAAAGTTTTAAATTATCATTTATT (Instability Sequence)
 TATTTTTTTTAAATGAGAGGGGAAAGCTGAAATTCCTTGTAAAGACACAAG
 GAAAAAGAATGGCCCTACTATTATCATGCAAAAATGCTTTGTTGGCACCT
 CAGATTAATCATATAATAGCTATAGTCTCTTCAGCATTTGTTTAAATTTT
 AGAAAACCTGTATAAATTACTGGTGCATAACTTAAAGATTATTCTGCCTT
 TGGCTAATTGAGTAATTCCTCCAGCACTAGAGACCGCTCAGTGCTCTT
 ACTAGATGAACTCAGTAACGCCTTGAGCTGGGTTGATTGAGGATGTGTGA
 AAAAGCTCACAGAGCCCGATGCCTGCTGCTATTTACGGCAATGAGCCTT
 TTTCTTTCTACACTGAAGATTTTCTTCTTATTTAATGTGGTTATTTTGG (Instability Sequence)
 GCTCAGAAATAATTGCTCTGTTGAAAATAATCCTTTGTCAGAAAAGAAGG
 TAGCTACCACATCATTTTGAAGGACCATGAGCAACTATAAGCAAAGCCA
 TAAGAAGTGTTTGATCGATATATTAGGGGTAGCTCTTGATTTTGTTAAC
 ATTAAGATAAGGTGACTTTTTCCCCCTGCTTTTAGGATTAATAATCAAAGA (Sub-optimal Poly-
 adenylation Site)
 TACTTCTATATTTTATCACTATAGATCATAGTTATTATACAATGTAGTG
 AGTCCTGCATGGGTACTCGATGTGTAATGAAACCTGAAATAATAATAAGA
 TAATAAGAAAAGCAATAATTTTCTAAAGCTGTGCTGTCGGTGATACAGAG
 ATGATACTCAAATTATAAATAAACTCTTCATTTTGTGAATTATAGAAGCT (Optimal Polyadeny-
 lation Site)
 ACTTTTTATAAAGCCATATTTTTTTAGGGAACTAAGGAGTGACATAGAA
 CTGATGAATGAGTAAAGTAAGTTTTTGCTGGATTTTTGTAGAAGTCTGGA
 CGTTGAGGATTCATTATGCTGTGGTTAACTTTAAATATTTTT

Fig. 2

COMPUTER PREDICTED DOMAINS
IN LABYRINTHIN

MVIALGVWTSVAVVWFDLVDDYEEVLGKLGIIYDADGDGDFDVDDAKVLLGLK

^

ERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIIDEAKEQIQSLLHEMVHAE

HVEGEDLQQEDGPTGEPQQEDDEFMATDVDDRFETLEPEVSHEETEHSYHV

EETVSQDCNQDMEEMMSEQENPDSSEPVEDERLHHD TDdvt yqv yeeqavY

<--MAD I-->

EPLENEGIEITEVTAPEDNPVEDSQviveevsifpvEEQQWCPPDT

^

<--MAD II-->

____ Predicted Ca⁺⁺ Binding Region

VLGKLGIIYDADGDGDFDVDDAKVLLGLK

Parvalbumin
Calmodulin
Troponin-C

vkafaiidqdksgfieedelklflqnf
fkeafslfdkdgdtittkelgtvmrsl
ladcfrvfdknadgfidieelgeilrat

Ca⁺⁺ Binding Residues
Required Residue

* * * * *

+

SYMBOL KEY

BOLD = eukaryotic Leader Sequence

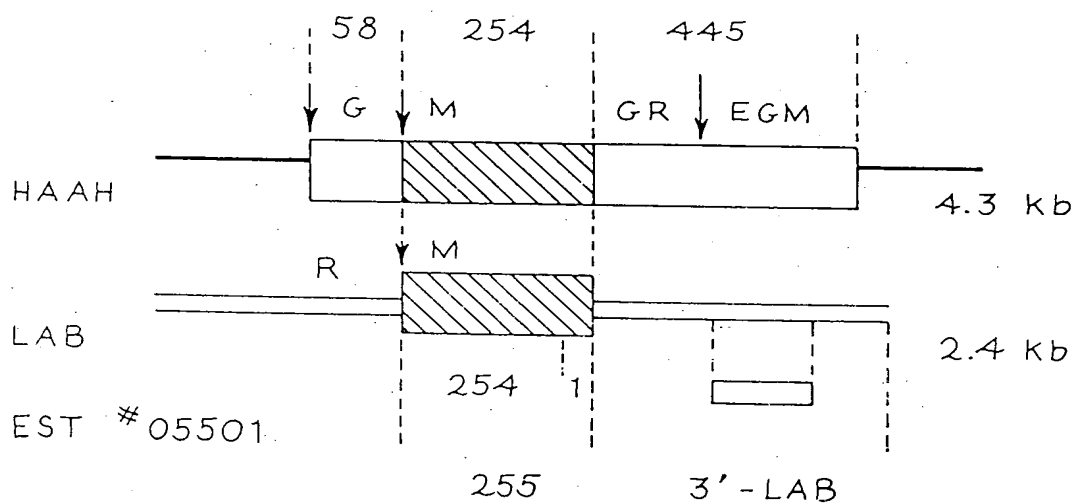
_____ = Myristylation site

^

lower case = Membrane Anchoring Domain (MAD)

<----->

3/3



↓ = START CODON
 R = RIBOSOME BINDING SITE
 E = ENZYMATIC SITE
 G = GLYCOSYLATION SITE
 M = MEMBRANE ANCHORING DOMAIN
 3'-LAB = CONTAINS POLY A SIGNAL (x2);
 INSTABILITY SEQUENCE (x4)

Fig. 3